

10/ 522096

Sequence listing
SEQUENCE LISTING

DT01 Rec'd PCT/ET 24 JAN 2005

<110> Ehrhardt, Thomas
Sonnewald, Uwe
Bornke, Frederik
Chen, Shuai

<120> Sucrose-6-Phosphate Phosphatase as Target for Herbicides

<130> 532622010200

<140> Not yet assigned

<141> 2005-01-24

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 1278

<212> DNA

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (1)..(1275)

<223>

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Asp	His	Thr	Met	Val	Asp	His	His	Asp	Ala	Glu	Asn	Leu	Ser	Leu	Leu	
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aga	ttt	aat	gct	tta	tgg	gag	gcg	aat	tat	cgt	gat	aac	tct	ttg	tta	144
Arg	Phe	Asn	Ala	Leu	Trp	Glu	Ala	Asn	Tyr	Arg	Asp	Asn	Ser	Leu	Leu	
		35				40						45				

gtg	ttc	tca	act	ggg	aga	tca	cca	aca	ctt	tac	aag	gag	ttg	agg	aaa	192
Val	Phe	Ser	Thr	Gly	Arg	Ser	Pro	Thr	Leu	Tyr	Lys	Glu	Leu	Arg	Lys	
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gaa ata aca tat ggt aac tct gtg gtg cct gat gat ggt tgg gaa gct Glu Ile Thr Tyr Gly Asn Ser Val Val Pro Asp Asp Gly Trp Glu Ala 85 90 95	288
ttt cta aat aac aag tgg gac aga aag ata gta aca gag gag act agc Phe Leu Asn Asn Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser 100 105 110	336
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act ctt tcc aag cgc ttc gaa gaa cgt ggg ctg gat gtc aaa ata att Thr Leu Ser Lys Arg Phe Glu Glu Arg Gly Leu Asp Val Lys Ile Ile 145 150 155 160	480
tac agt gga ggc atg gat cta gat ata tta cca caa ggt gct ggc aaa Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys 165 170 175	528
gga caa gca ctt gca tat ttg ctt aag aaa ttg aag agt gag gga aaa Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys 180 185 190	576
tta cca aac aac acc ctt gcc tgt ggt gac tct ggg aat gat gct gag Leu Pro Asn Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu 195 200 205	624
cta ttc agt atc cca gat gtg tat ggt gta atg gta gct aat gca cag Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln 210 215 220	672
gag gaa tta ttg caa tgg cat gct gca aat gcg aag aat aat cct aaa Glu Glu Leu Leu Gln Trp His Ala Ala Asn Ala Lys Asn Asn Pro Lys 225 230 235 240	720
gta att cat gca aca gag agg tgt gct gcc ggt atc ata caa gct att Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile 245 250 255	768
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Sequence listing

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Thr Leu Phe Gly Thr Cys His Gly Asp Lys Gln Gly Lys Gln Phe Arg	
340 345 350	
att tgg gtc gat caa gtt tta cct gta cag gtt ggt tcg gac tca tgg	1104
Ile Trp Val Asp Gln Val Leu Pro Val Gln Val Gly Ser Asp Ser Trp	
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Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Arg Arg Cys	
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tgc ata act aca gtc cta tta agt tca aag aat aag act gtc gca gat	1200
Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Lys Thr Val Ala Asp	
385 390 395 400	
gga ctc act tgg acc cac gta cat cag aca tgg ctg aat gga gct gca	1248
Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu Asn Gly Ala Ala	
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<213> Nicotiana tabacum

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35 40 45

Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
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Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr
65 70 75 80

Glu Ile Thr Tyr Gly Asn Ser Val Val Pro Asp Asp Gly Trp Glu Ala

Sequence listing
90

85

95

Phe	Leu	Asn	Asn 100	Lys	Trp	Asp	Arg	Lys 105	Ile	Val	Thr	Glu	Glu 110	Thr	Ser
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Thr 145	Leu	Ser	Lys	Arg	Phe 150	Glu	Glu	Arg	Gly	Leu 155	Asp	Val	Lys	Ile	Ile 160
Tyr	Ser	Gly	Gly	Met 165	Asp	Leu	Asp	Ile	Leu 170	Pro	Gln	Gly	Ala	Gly 175	Lys
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Leu	Pro	Asn 195	Asn	Thr	Leu	Ala	Cys 200	Gly	Asp	Ser	Gly	Asn 205	Asp	Ala	Glu
Leu	Phe 210	Ser	Ile	Pro	Asp	Val 215	Tyr	Gly	Val	Met	Val 220	Ala	Asn	Ala	Gln
Glu 225	Glu	Leu	Leu	Gln	Trp 230	His	Ala	Ala	Asn	Ala 235	Lys	Asn	Asn	Pro	Lys 240
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Gly	His	Ser	Asn 260	Leu	Gly	Pro	Ser	Thr 265	Ser	Pro	Arg	Asp	Val 270	Met	Asp
Leu	Ser	Asp 275	Cys	Lys	Met	Glu	Asn 280	Phe	Val	Pro	Ala	Tyr 285	Glu	Val	Val
Lys	Phe 290	Tyr	Leu	Phe	Phe	Glu 295	Lys	Trp	Arg	Arg	Gly 300	Glu	Ile	Glu	His
Ser 305	Glu	His	Tyr	Leu	Ser 310	Asn	Leu	Lys	Ala	Val 315	Cys	Arg	Pro	Ser	Gly 320
Thr	Phe	Val	His	Pro 325	Ser	Gly	Val	Glu	Lys 330	Ser	Leu	Gln	Glu	Cys 335	Val

Sequence listing

Thr Leu Phe Gly Thr Cys His Gly Asp Lys Gln Gly Lys Gln Phe Arg
340 345 350

Ile Trp Val Asp Gln Val Leu Pro Val Gln Val Gly Ser Asp Ser Trp
355 360 365

Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Arg Arg Cys
370 375 380

Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Lys Thr Val Ala Asp
385 390 395 400

Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu Asn Gly Ala Ala
405 410 415

Ala Ser Asp Ser Ala Ser Trp Phe Phe
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<211> 1278

<212> DNA

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Asp	His	Thr	Met	Val	Asp	His	His	Asp	Pro	Glu	Asn	Leu	Ser	Leu	Leu	
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agg	ttt	aat	gct	tta	tgg	gag	gcc	aat	tat	cgt	gaa	aac	tcc	ttg	tta	144
Arg	Phe	Asn	Ala	Leu	Trp	Glu	Ala	Asn	Tyr	Arg	Glu	Asn	Ser	Leu	Leu	
		35					40					45				

gtg	ttc	tca	act	ggg	aga	tca	cct	acc	ctt	tac	aag	gag	ttg	aga	aaa	192
Val	Phe	Ser	Thr	Gly	Arg	Ser	Pro	Thr	Leu	Tyr	Lys	Glu	Leu	Arg	Lys	
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gag	aag	ccc	atg	cta	acc	cca	gat	att	acc	att	atg	tct	gtg	ggg	act	240
Glu	Lys	Pro	Met	Leu	Thr	Pro	Asp	Ile	Thr	Ile	Met	Ser	Val	Gly	Thr	

Sequence listing																
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aaa Lys	ttt Phe	cct Pro 115	gaa Glu	ctc Leu	acc Thr	ctt Leu	cag Gln 120	tca Ser	gaa Glu	aca Thr	gag Glu	cag Gln 125	cga Arg	cca Pro	cac His	384
aag Lys	gtc Val 130	agt Ser	ttc Phe	tat Tyr	gtt Val	cag Gln 135	aaa Lys	gac Asp	aag Lys	gct Ala	caa Gln 140	gat Asp	ata Ile	acg Thr	gga Gly	432
act Thr 145	ctt Leu	tcc Ser	aag Lys	cgc Arg	ttg Leu 150	gaa Glu	gaa Glu	cgt Arg	ggg Gly	ttg Leu 155	gat Asp	gtc Val	aaa Lys	ata Ile	att Ile 160	480
tat Tyr	agc Ser	gga Gly	ggg Gly	atg Met 165	gat Asp	ttg Leu	gac Asp	att Ile	ttg Leu 170	cca Pro	caa Gln	ggt Gly	gct Ala	ggc Gly 175	aaa Lys	528
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ctt Leu	ttc Phe 210	agt Ser	atc Ile	cca Pro	gat Asp	gtt Val 215	tat Tyr	ggt Gly	gtg Val	atg Met	gta Val 220	gcg Ala	aat Asn	gca Ala	cag Gln	672
gag Glu 225	gag Glu	tta Leu	tta Leu	caa Gln	tgg Trp 230	cgt Arg	gct Ala	gca Ala	aat Asn	gca Ala 235	aaa Lys	gat Asp	agt Ser	cca Pro	aaa Lys 240	720
gta Val	att Ile	cat His	gca Ala	aca Thr 245	gag Glu	aga Arg	tgt Cys	gcc Ala	gcg Ala 250	ggt Gly	ata Ile	ata Ile	caa Gln	gca Ala 255	att Ile	768
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atg Met	tca Ser	gac Asp 275	tgc Cys	aag Lys	atg Met	gag Glu	aat Asn 280	ttt Phe	gtt Val	cct Pro	gct Ala	tat Tyr 285	gaa Glu	gtc Val	gtc Val	864
aaa Lys	ttt Phe 290	tac Tyr	ttg Leu	ttt Phe	ttc Phe	gag Glu 295	aaa Lys	tgg Trp	agg Arg	cgt Arg	gga Gly 300	gaa Glu	att Ile	gag Glu	aat Asn	912
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Sequence listing

Thr	Phe	Val	His	Pro	Ser	Gly	Val	Glu	Lys	Tyr	Leu	Glu	Asp	Cys	Ile	
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tta	gtg	agt	ttc	aag	aaa	tgg	gag	ctt	tgt	ggc	gaa	gag	cga	caa	tgt	1152
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Gly	Leu	Thr	Trp	Thr	His	Val	His	Gln	Thr	Trp	Leu	Gln	Gly	Ala	Ala	
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gca	agt	gac	tcc	gcg	tcc	tgg	ttc	ttt	taa							1278
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<212> PRT

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Arg	Phe	Asn	Ala	Leu	Trp	Glu	Ala	Asn	Tyr	Arg	Glu	Asn	Ser	Leu	Leu	
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Val	Phe	Ser	Thr	Gly	Arg	Ser	Pro	Thr	Leu	Tyr	Lys	Glu	Leu	Arg	Lys	
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Glu	Lys	Pro	Met	Leu	Thr	Pro	Asp	Ile	Thr	Ile	Met	Ser	Val	Gly	Thr	
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Glu	Ile	Thr	Tyr	Gly	Asn	Ser	Met	Glu	Pro	Asp	Asp	Gly	Trp	Glu	Ala	
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Sequence listing

Phe Leu Asn Asp₁₀₀ Lys Trp Asp Arg Lys₁₀₅ Ile Val Thr Glu₁₁₀ Thr Ser
 Lys Phe Pro₁₁₅ Glu Leu Thr Leu Gln₁₂₀ Ser Glu Thr Glu Gln₁₂₅ Arg Pro His
 Lys Val₁₃₀ Ser Phe Tyr Val Gln₁₃₅ Lys Asp Lys Ala Gln₁₄₀ Asp Ile Thr Gly
 Thr₁₄₅ Leu Ser Lys Arg Leu₁₅₀ Glu Glu Arg Gly Leu₁₅₅ Asp Val Lys Ile Ile₁₆₀
 Tyr Ser Gly Gly Met₁₆₅ Asp Leu Asp Ile Leu₁₇₀ Pro Gln Gly Ala Gly₁₇₅ Lys
 Gly Arg Ala Leu₁₈₀ Ala Tyr Leu Leu Lys₁₈₅ Lys Leu Lys Ser Glu₁₉₀ Gly Lys
 Leu Pro Asn₁₉₅ Asn Thr Leu Ala Cys₂₀₀ Gly Asp Ser Gly Asn₂₀₅ Asp Ala Glu
 Leu Phe₂₁₀ Ser Ile Pro Asp Val₂₁₅ Tyr Gly Val Met Val₂₂₀ Ala Asn Ala Gln
 Glu₂₂₅ Glu Leu Leu Gln Trp₂₃₀ Arg Ala Ala Asn Ala₂₃₅ Lys Asp Ser Pro Lys₂₄₀
 Val Ile His Ala Thr₂₄₅ Glu Arg Cys Ala Ala₂₅₀ Gly Ile Ile Gln Ala₂₅₅ Ile
 Gly His Phe Asn₂₆₀ Leu Gly Pro Asn Thr₂₆₅ Ser Pro Arg Asp Val₂₇₀ Thr Asp
 Met Ser Asp₂₇₅ Cys Lys Met Glu Asn₂₈₀ Phe Val Pro Ala Tyr₂₈₅ Glu Val Val
 Lys Phe₂₉₀ Tyr Leu Phe Phe Glu₂₉₅ Lys Trp Arg Arg Gly₃₀₀ Glu Ile Glu Asn
 Ser₃₀₅ Asp Leu His Leu Ser₃₁₀ Asn Leu Lys Ala Val₃₁₅ Cys Arg Pro Ser Gly₃₂₀
 Thr Phe Val His Pro₃₂₅ Ser Gly Val Glu Lys₃₃₀ Tyr Leu Glu Asp Cys₃₃₅ Ile
 Asn Thr Leu Arg₃₄₀ Thr Cys His Gly Asp₃₄₅ Lys Gln Gly Lys Gln₃₅₀ Phe Arg

Sequence listing

Ile Trp Val Asp Leu Val Leu Pro Thr Gln Val Gly Ser Asp Ser Trp
355 360 365

Leu Val Ser Phe Lys Lys Trp Glu Leu Cys Gly Glu Glu Arg Gln Cys
370 375 380

Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Val Thr Val Ala Asp
385 390 395 400

Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu Gln Gly Ala Ala
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Ala Ser Asp Ser Ala Ser Trp Phe Phe
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ctg ctt agg ttc aat gct tta tgg gaa gcc aat tat cgt gat aac tct 207
Leu Leu Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Asp Asn Ser
35 40 45

ttg tta gtg ttc tct act ggg aga tca cct aca ctt tac aag gaa tta 255
Leu Leu Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu
50 55 60

agg aaa gaa aag ccc atg cta acc cca gat att aca att atg tct gtg 303
Arg Lys Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val
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gga Gly	act Thr	gaa Glu	ata Ile	aca Thr	tat Tyr	ggt Gly	aac Asn	gct Ala	atg Met	gtg Val	cct Pro	gat Asp	gat Asp	ggt Gly	tgg Trp	351
	80					85					90					
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95					100					105					110	
aca Thr	agc Ser	aag Lys	ttt Phe	cct Pro	gaa Glu	ctc Leu	agt Ser	ctg Leu	cag Gln	tca Ser	gaa Glu	aca Thr	gag Glu	cag Gln	cga Arg	447
				115					120					125		
cca Pro	cac His	aag Lys	gtc Val	agt Ser	ttc Phe	tat Tyr	gtt Val	cag Gln	aaa Lys	gag Glu	aaa Lys	gct Ala	caa Gln	gat Asp	ata Ile	495
			130					135					140			
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		145					150					155				
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	160					165					170					
ggc Gly	aaa Lys	gga Gly	caa Gln	gca Ala	ctt Leu	gca Ala	tat Tyr	ctg Leu	ctt Leu	aag Lys	aaa Lys	ctg Leu	aag Lys	agc Ser	gag Glu	639
175					180					185					190	
gga Gly	aaa Lys	tta Leu	cca Pro	agc Ser	aac Asn	acc Thr	ctt Leu	gcc Ala	tgc Cys	ggc Gly	gac Asp	tcc Ser	ggg Gly	aat Asn	gac Asp	687
				195					200					205		
gct Ala	gaa Glu	tta Leu	ttc Phe	agt Ser	atc Ile	cca Pro	gat Asp	gtg Val	tat Tyr	ggt Gly	gta Val	atg Met	gta Val	gct Ala	aat Asn	735
			210					215					220			
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		225					230					235				
ccc Pro	aaa Lys	gta Val	att Ile	cat His	gca Ala	tca Ser	gag Glu	agg Arg	tgt Cys	gcc Ala	gcc Ala	ggt Gly	atc Ile	ata Ile	caa Gln	831
	240					245				250						
gcc Ala	att Ile	ggt Gly	cat His	ttc Phe	aaa Lys	cta Leu	ggt Gly	cca Pro	agt Ser	acc Thr	tcc Ser	cca Pro	aga Arg	gac Asp	gtt Val	879
255					260					265					270	
acg Thr	gat Asp	ttg Leu	tca Ser	gat Asp	tgc Cys	aag Lys	atg Met	gac Asp	aac Asn	ttt Phe	gtt Val	cct Pro	gcc Ala	tat Tyr	gaa Glu	927
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gag Glu	cat His	tct Ser	gag Glu	cat His	tat Tyr	ctg Leu	cca Pro	aac Asn	ctg Leu	aaa Lys	gca Ala	gtg Val	tgt Cys	ata Ile	cca Pro	1023
		305					310					315				
tct Gly	ggt Thr	act Thr	ttt Phe	gtt Leu	cac Gln	cca Pro	tct Gly	ggt Thr	gtt Leu	gag Glu	aaa Lys	tcc Ser	ctt Gln	cag Gln	gaa Glu	1071

Sequence listing

Ser Gly Thr Phe Val His Pro Ser Gly Val Glu Lys Ser Leu Gln Glu
 320 325 330

tgt gta act tca ttc gga aca tgt cat gct gac aag cag ggg aaa caa 1119
 Cys Val Thr Ser Phe Gly Thr Cys His Ala Asp Lys Gln Gly Lys Gln
 335 340 345 350

tat cgt gtt tgg gtc gat caa gtt tta cct tca cag gtt ggt tca gac 1167
 Tyr Arg Val Trp Val Asp Gln Val Leu Pro Ser Gln Val Gly Ser Asp
 355 360 365

tca tgg tta gtg agt ttc aag aag tgg gag ctc tct ggt gaa gac atg 1215
 Ser Trp Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Met
 370 375 380

cga tgc tgc ata acc aca gtc cta tta agt tca aag aat aag act gtt 1263
 Arg Cys Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Lys Thr Val
 385 390 395

gca gac ggg ctc act tgg act cac gta cat cag aca tgg ctg cac ggt 1311
 Ala Asp Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu His Gly
 400 405 410

gat gca gca agt gac tcc gca acc tgg ttc ttt tagattgtca tctcagtgtgta 1364
 Asp Ala Ala Ser Asp Ser Ala Thr Trp Phe Phe
 415 420 425

ttaactctga aaattccgca cccctttttac cagttcacac ccagaataaa cacaacatac 1424

aaactatagt tgataatcaa tgtattaact ttctccttct ttgataatca atgtattgcc 1484

atctaaacca gtgaagatgg ctttatcttt tgtgtagtat aaagaattat attagtatca 1544

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<400> 6

Met Asp Arg Leu Thr Ser Ala Ala Arg Leu Met Ile Val Ser Asp Leu
 1 5 10 15

Asp His Thr Met Val Asp His His Asp Ser Glu Asn Leu Ser Leu Leu
 20 25 30

Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Asp Asn Ser Leu Leu
 35 40 45

Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys

Sequence listing
60

50

55

Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr
65 70 75 80

Glu Ile Thr Tyr Gly Asn Ala Met Val Pro Asp Asp Gly Trp Glu Thr
85 90 95

Phe Leu Asn Asn Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser
100 105 110

Lys Phe Pro Glu Leu Ser Leu Gln Ser Glu Thr Glu Gln Arg Pro His
115 120 125

Lys Val Ser Phe Tyr Val Gln Lys Glu Lys Ala Gln Asp Ile Met Lys
130 135 140

Thr Leu Ser Lys Arg Leu Glu Glu Arg Gly Leu Asp Val Lys Ile Ile
145 150 155 160

Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys
165 170 175

Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys
180 185 190

Leu Pro Ser Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu
195 200 205

Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln
210 215 220

Lys Glu Leu Leu Gln Trp His Ala Ala Asn Ala Lys Asn Asn Pro Lys
225 230 235 240

Val Ile His Ala Ser Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
245 250 255

Gly His Phe Lys Leu Gly Pro Ser Thr Ser Pro Arg Asp Val Thr Asp
260 265 270

Leu Ser Asp Cys Lys Met Asp Asn Phe Val Pro Ala Tyr Glu Val Val
275 280 285

Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile Glu His
290 295 300

Sequence listing

Ser Glu His Tyr Leu Pro Asn Leu Lys Ala Val Cys Ile Pro Ser Gly
305 310 315 320

Thr Phe Val His Pro Ser Gly Val Glu Lys Ser Leu Gln Glu Cys Val
325 330 335

Thr Ser Phe Gly Thr Cys His Ala Asp Lys Gln Gly Lys Gln Tyr Arg
340 345 350

Val Trp Val Asp Gln Val Leu Pro Ser Gln Val Gly Ser Asp Ser Trp
355 360 365

Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Met Arg Cys
370 375 380

Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Lys Thr Val Ala Asp
385 390 395 400

Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu His Gly Asp Ala
405 410 415

Ala Ser Asp Ser Ala Thr Trp Phe Phe
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<213> Solanum tuberosum

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tatagagcca ctatatatat acatattctc gattatatat gtaaattgagt tacccttttt 180

ttccacttaa attatatag 199

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Sequence listing

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<212> DNA

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<223> Primer

<400> 9

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47

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Sequence listing

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27

<210> 15

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Sequence listing

<223> Primer

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<210> 16

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<223> Primer

<400> 16

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23

<210> 17

<211> 23

<212> DNA

<213> Artificial sequence

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<223> Primer

<400> 17

gcctttgcaa tccacatctg ttg

23

<210> 18

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<212> DNA

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<210> 19

Sequence listing

<211> 33

<212> DNA

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<223> Primer

<400> 19

gtcgacctaa aagaaccagg acgcggagtc act

33